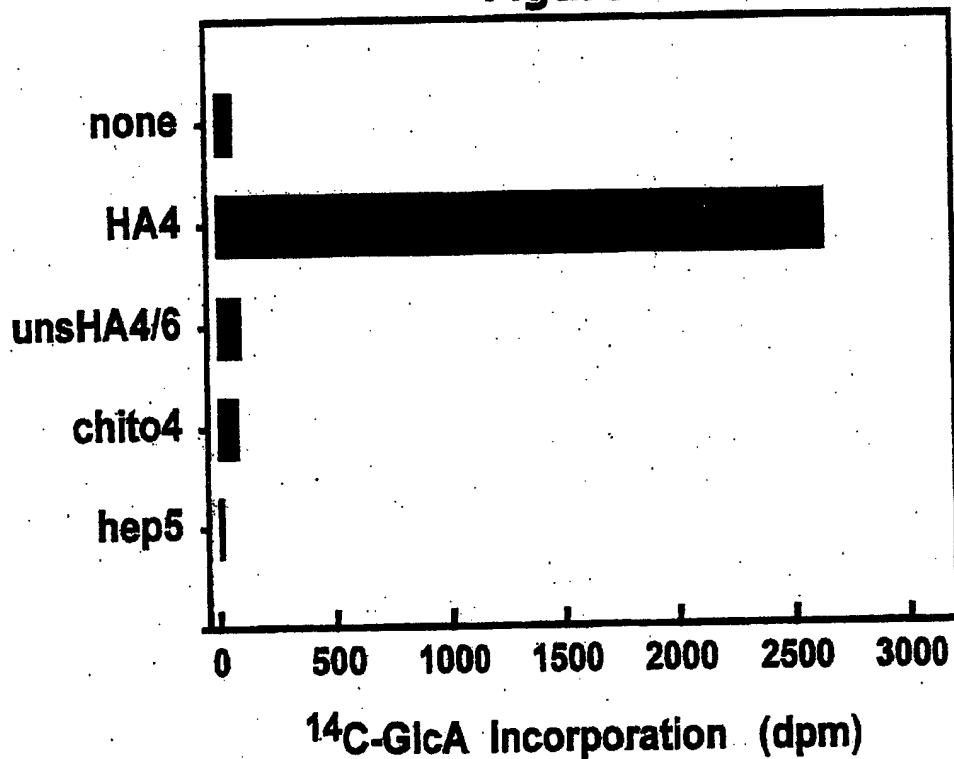
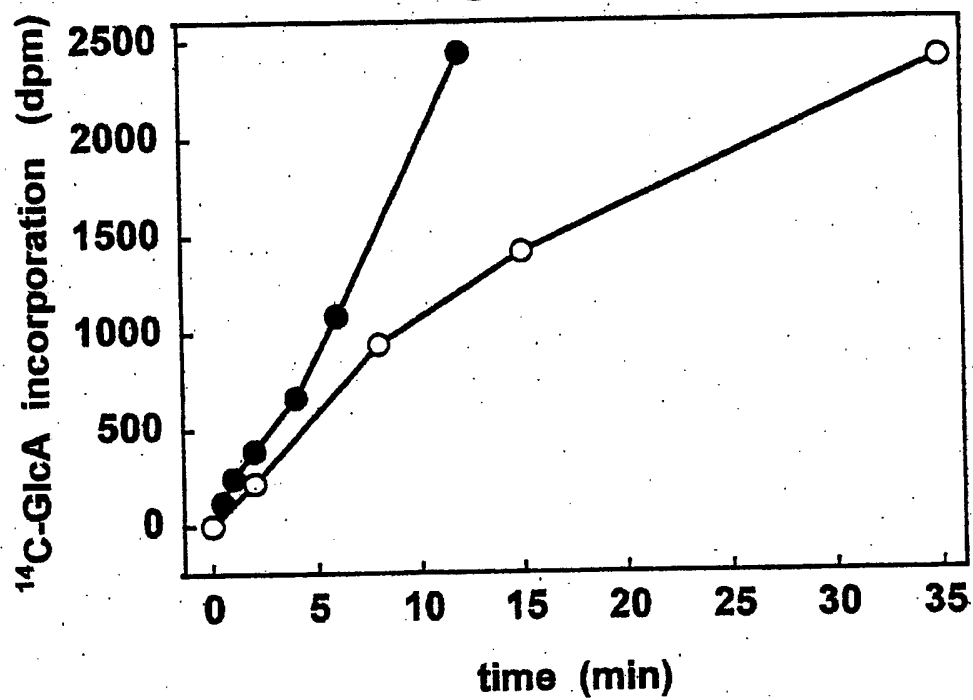
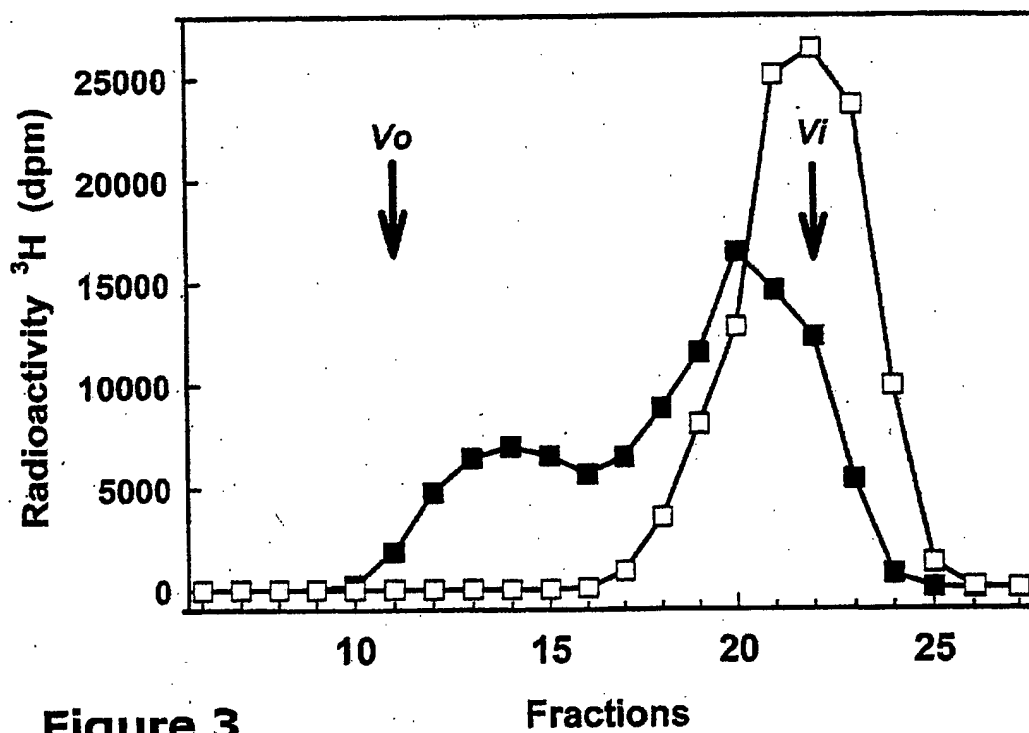


**Figure 1**

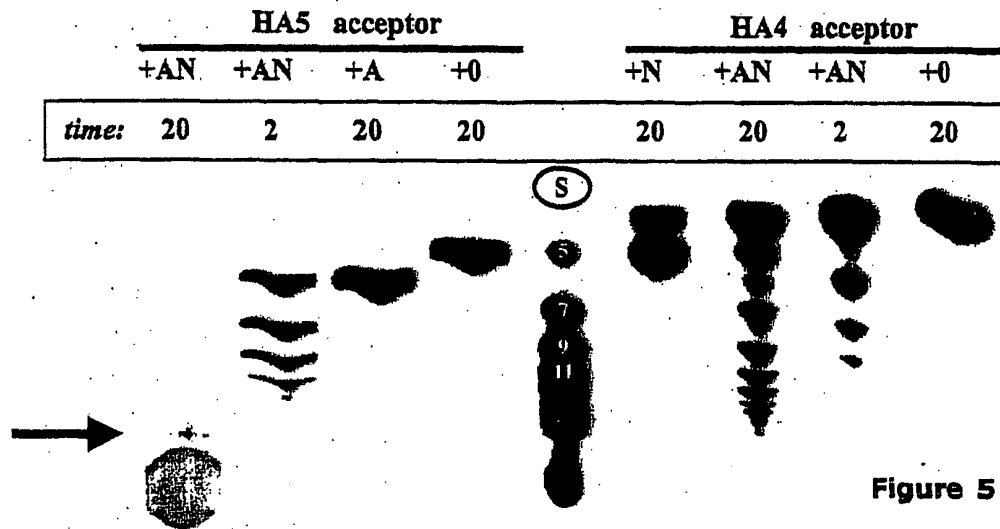


**Figure 2**



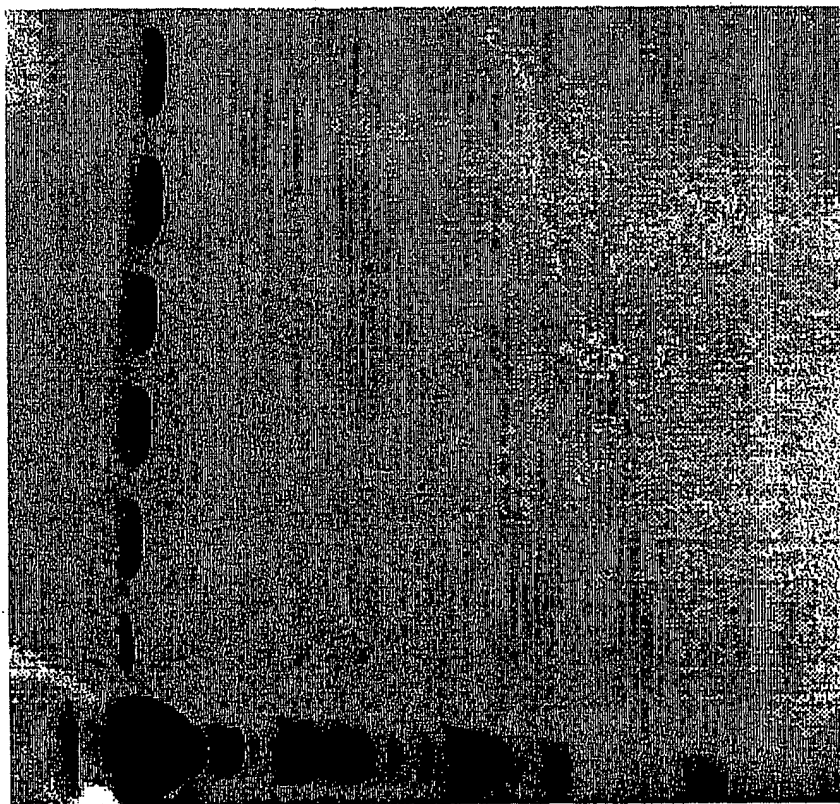




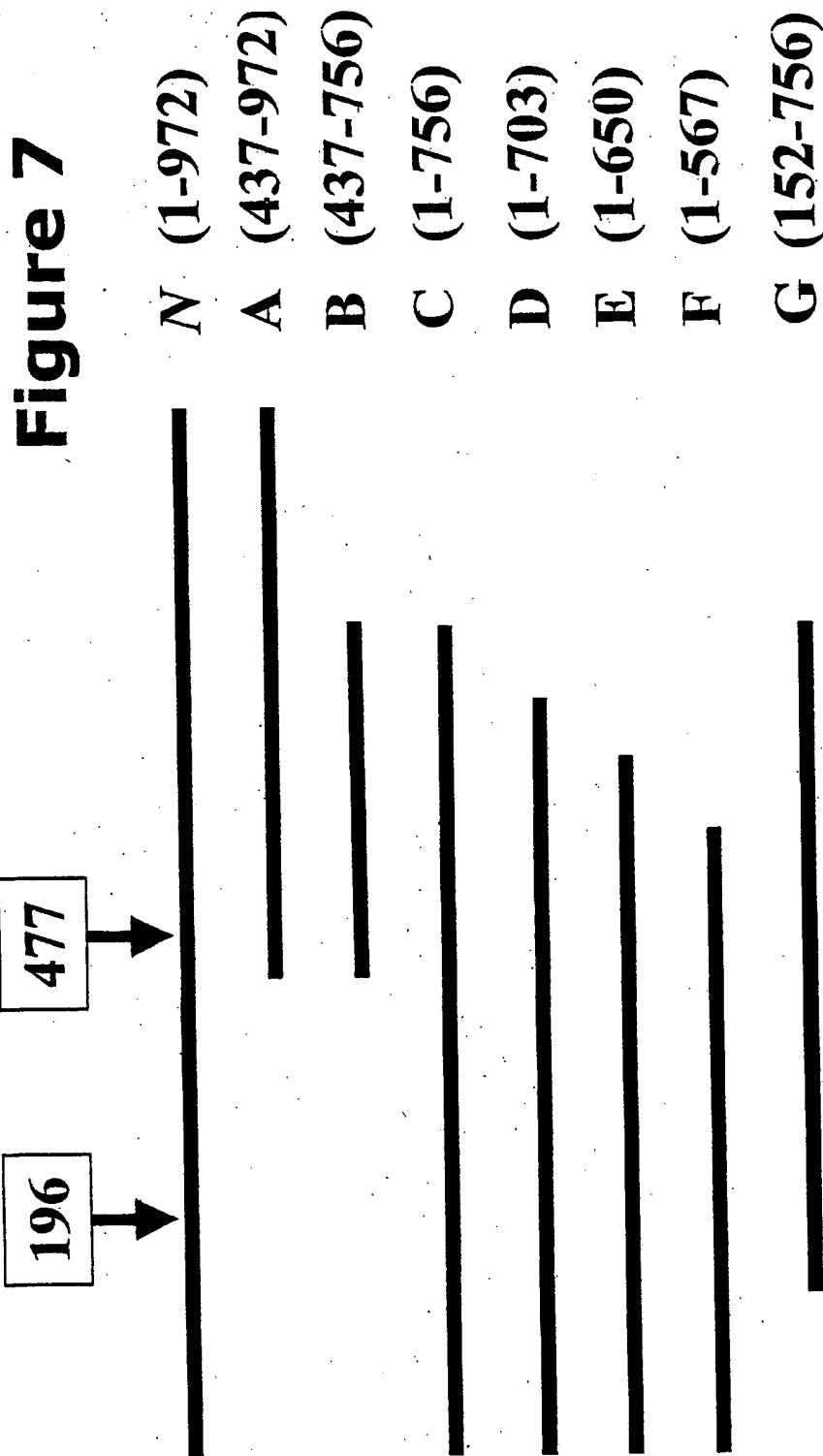


# Ion Gel Filtration

## Ex Fractions



**Figure 6**



*GlcNAc- Tase*      *GlcUA- Tase*      *Membrane association*

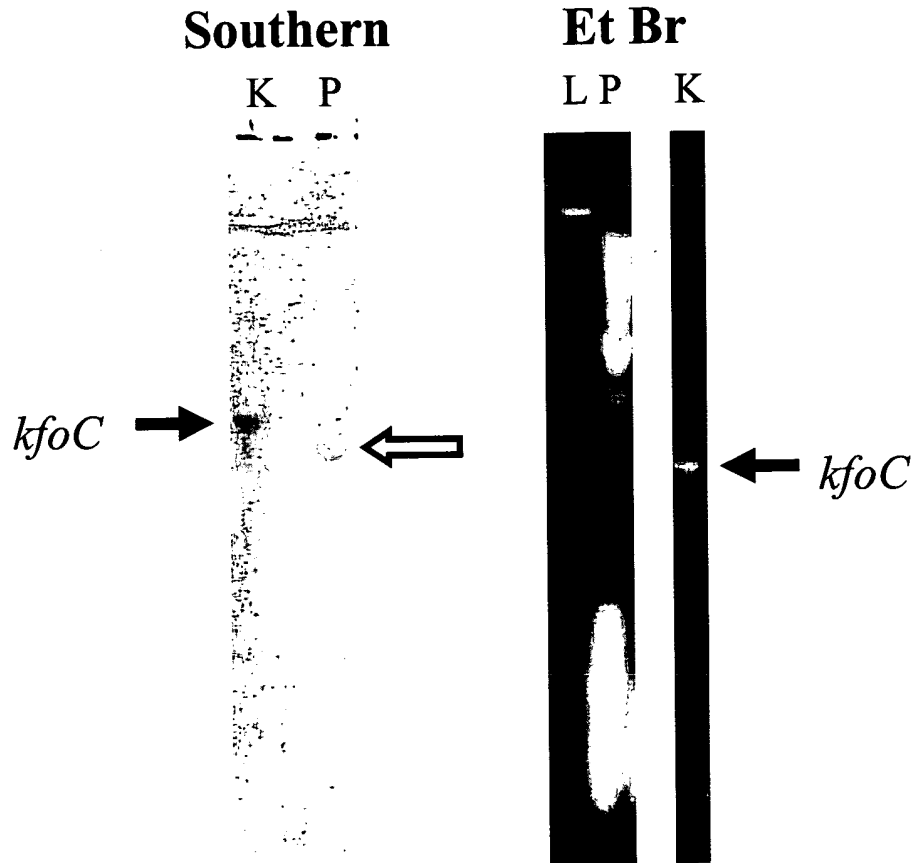


FIG. 8



**Figure 9**

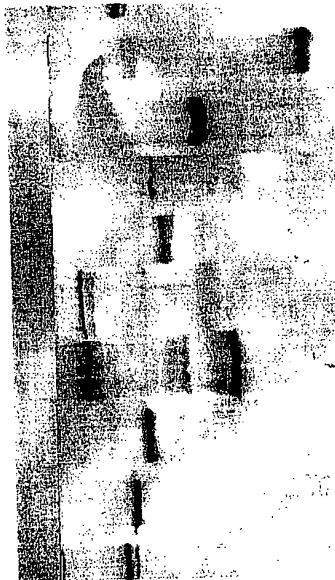


Figure 10

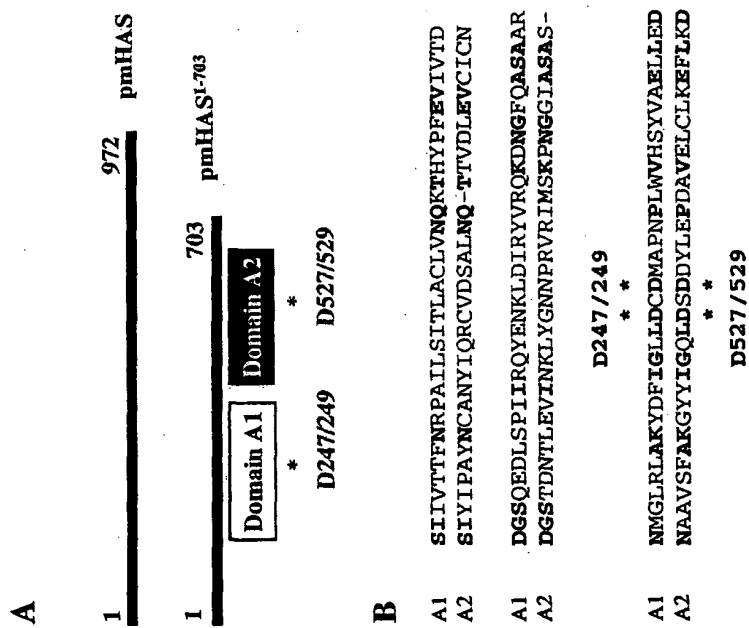


Figure 11

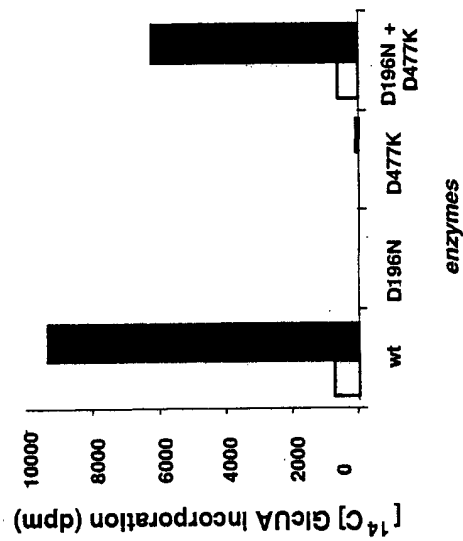


Figure 12

pmCS	1	MNTLSQAIKA	YNSNDYELAL	KLFERSAETY	GRKIVETQII	KCKEKLSTNS	50
pmHAS		-----	-----Q-----	-----I-----	-----T-----	-----AHP-----	
pmCS	51	YVS-----	EDKKNVCDSS	SDIATQILL	SNVKELTISE	SEKNSLAKKW	100
pmHAS		S-NSAHLSVN	KEE-VN----	F-----	-----V--D-----	-----T-----	
pmCS	101	KBITGKKSEN	AEIRKVELVP	KDFPKDIVLA	FLPDHVNDFT	WYKNNRKKSG	150
pmHAS		-LL-E-----	--V-A-A----	-----	-----	---K---R--	
pmCS	151	IKFVNKNIGL	SLIPTFNRS	RILDITDACL	VNOKTNYEPE	VVVADDGSEK	200
pmHAS		---EQHV--	---VT-----	A--S-----	-----H-----	-I-T---Q-	
pmCS	201	NELTIVORYE	QRLDIKYVRO	KDYGYQLCAV	RNLGLRTAKY	DYVSILDCDM	250
pmHAS		D-SP-IRQ--	N---R-----	--N-F-RS-A	--M--L---	---IGL---	
pmCS	251	APQQLWVHSY	LTELLEDNDI	VLIGPRKYVD	THNITAEQFL	NDPYLIESLP	300
pmHAS		--NP-----	VA-----D-L	TI-----I-	-QH-DPKD--	-NAS-L----	
pmCS	301	ETATNNNPSI	TSKGNISLDW	RLEHTAKTON	LRIGDSPTRY	FVAGNVAFSK	350
pmHAS		-VK---SVAA	KGE-TV-----	---Q-T--E-	---S-----	-A-----A-	
pmCS	351	EWLNKVGWFD	EETNNWGGED	VEFGYALEAK	GCEFRVIDGG	MAIHQEPFGK	400
pmHAS		K-----S-F--	-----	-----R-	-S--RT--I-	---Y-----	
pmCS	401	ENETEREACK	SITLKIYKER	VPYTYRKLIF	IEDSHIRIP	LVSIVIPAYN	450
pmHAS		-----D-----	N---D-MR--	-----	-----N-V-	-----	
pmCS	451	CANYIQRCVD	SALNQTVDL	EVCICNDGST	DNTLEVINKL	YGNNPRVRIM	500
pmHAS		-----	-----	-----	-----	-----	
pmCS	501	SKFNGGIASA	SNAAVSFARG	YYIGQLDSDD	YLEPDAVELC	EKEFLDKCTL	550
pmHAS		-----	-----	-----	-----	-----	
pmCS	551	ACVYITNRNV	NPDGSLIANG	YNWPEFSREK	LTAMLAHHT	RMFTIRAWLL	600
pmHAS		-----	-----	-----	-----	-----	
pmCS	601	TGGFNENIEN	AVDYDMFLKL	SEVGKFKHIN	KICYNRVLHG	DNTSIXKLDY	650
pmHAS		-----K-----	-----	-----	-----	-----	
pmCS	651	QKKNHFFVVN	QSLNRQGTNY	YNYDRFDDLD	ESRKVIIFNKT	AEYQREMDML	700
pmHAS		-----	-----T-----	-----E-----	-----	---I-I---	
pmCS	701	KDLKLIONKD	AKLAVSITYP	NTINGLVKKL	NMIEYNNKI	FVILHVDKN	750
pmHAS		--I-I-----	-----	-----	-----	---V-----	
pmCS	751	HLTFDIKKEI	LAFYHKHQVN	ILLNNDISYY	TSMRLIKTEA	HLNINIKLSQ	800
pmHAS		-----	-----	-----	-----	-----	
pmCS	801	LNLNCEYIIF	DNHDSLFVEN	DSYAYMKKYD	VGMNESALTH	DWIEKINARF	850
pmHAS		-----	-----	-----	-----	-----	
pmCS	851	PFKKLIKTYF	NNDNLRSMNV	KGASQGMFMK	YALPHELLTI	IKKVITSQCS	900
pmHAS		-----	---K-----	-----T-----	---A-----	-----	
pmCS	901	IDSVPEYNTE	DIWFQFALLI	LEKKIGHVFN	KTSLTLYMPW	ERKLQWTEQ	950
pmHAS		-----	-----	-----	-----	-----	
pmCS	951	IQBAKKGANI	PVKRFIINSI	TL			972
pmHAS		-E---R-----	-----	---			

Figure 13

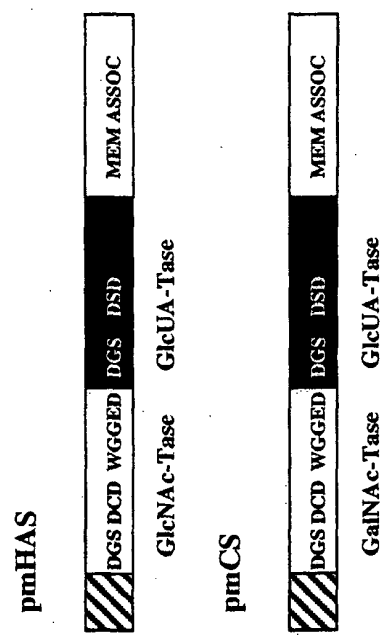


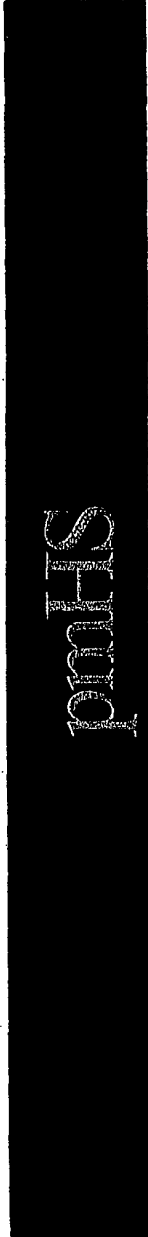
Figure 14

91	140
HS1	APPLVSIIMTSHNTEKFEASINSLLOTTYNNEVIVVDDYSTDKTFQIA
KfiC	GKDLVSIIMSVFENSEDTIAYSLHLLNQTYENIEILVCDDCSSDKSLEII
con	...LVSIIM*.N*.E..I..S..SLL.QTY#N.E!.V.DD.S*DK*.#I.
141	190
HS1	SRIANSTSKVKTFRINSNLGTYFAKNTGILKSKGDI IFFQBSDDVCHHER
KfiC	KSIAYSSSRVKVYSSRKNQGPYNIRNELIKKAHGNFITFQDADDLSHPER
con	..IA.S*S*VK.%....N.G.Y...N..I.K..G#.I.FQD.DD..H.ER
191	240
HS1	IERCVNALLSNKDNIAVRCAYSRINLETQNI IKVNDNKYKLGILITLGVYR
KfiC	IQRQVEVLRNNKAVICM.ANWIRVASNGKIQFFYDDKATRMSVWSSMIKK
con	I#R.V#.L..NK..I.....R!..#.....#D....*\$...!*...!.*
441	490
HS2	YITCDDDIRYPADYINTMIKKINKYND.KAAIGLHGVIFPSRVNKFYSSD
KfiA	IVLTDDDDIIYPPDYVEKMLNFYNSEFAIENCIVGIHGCIIYIDAFDGD.QSK
con	...DDDI.YP.DY!#M....N.%.....!G.HG.I%.....#.....S.
491	540
HS2	RIVYNFQKTRKDTAVNLTGTVAFRVSIFNKFSLSDFEHPGMVDIYFS
KfiA	RKVFSFTQGLLRPRVNVQLGTGTVFLKADQLPSLKYMDGSQR.FVDVRES
con	R.V%.F.....*.VN.LGTGTV.*.....D.....VD!.FS

Figure 14 cont'd

1

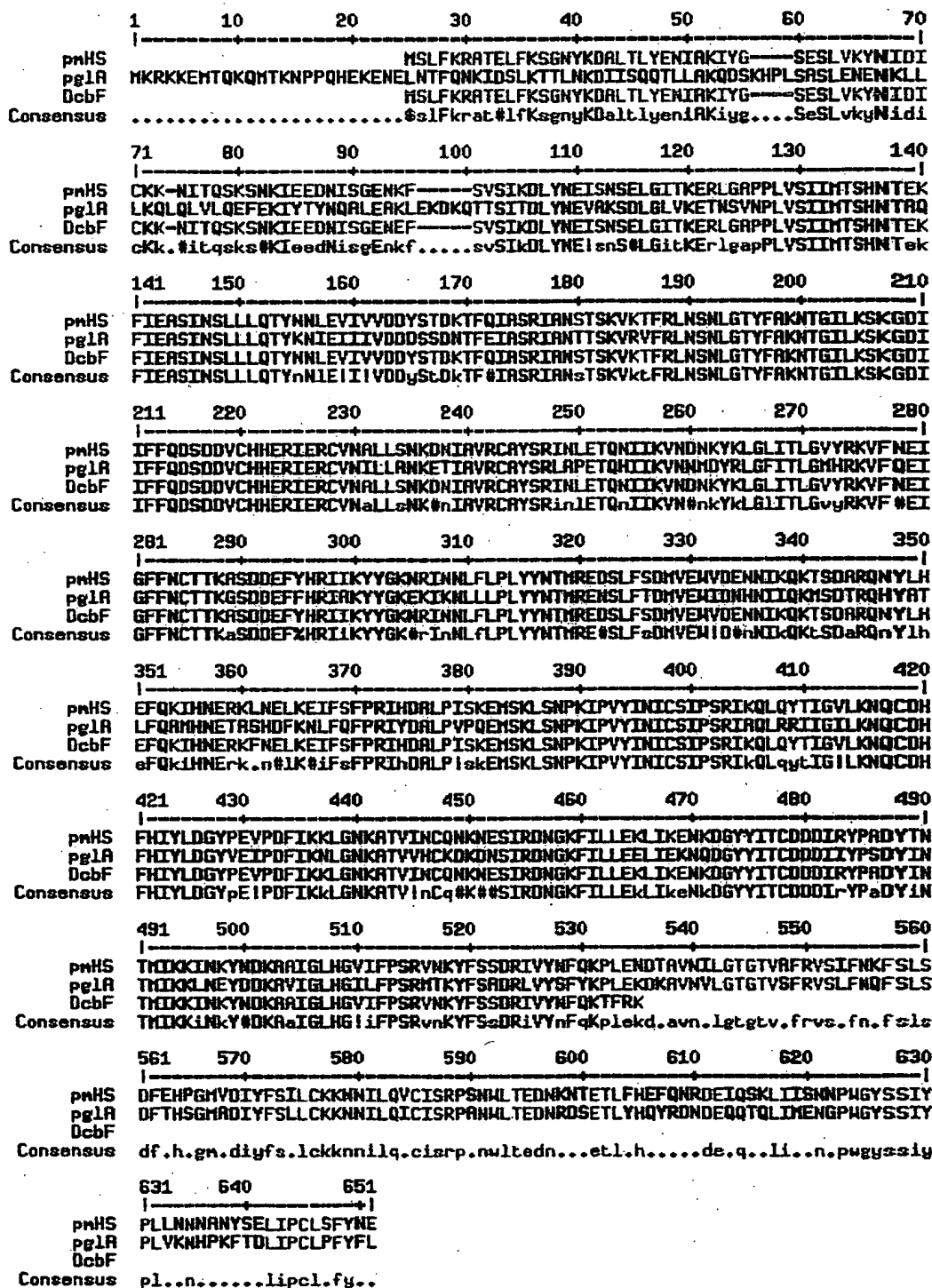
617



	1	10	20	30	40	50	60	70
KF1C								
HSR1	GKDLVSIINSVENSEDIAYSLHSLLNQTYENIELVCDDSSDKSELIKSJAYSRRVKYSSRKHQG							
kf1A	APPLYSIHTSHNTEKFIEASLHSLLLQTNNLEVTVDYSDTKTFIQASRIANSTSKVKTFRLSNLG							
HSR2	NLVANNSSYPPRKKELVNSIQSLHAQV-DKNILCLNEFEETPEELDGFSLNPVI-----POKYDYDVG							
Consensus	IPYYINICISPSRIKQLQYTIGVLKHQC-DNFHLYLDGYEVPDFIKKLGNKATVINCAQNKNESIDHG							
	. . p.v.nl.s.p.r.k.l.y.s.i.sl.nq.#.i.i.l.....e.p.l....s.a.vi.....s.k#.g.							
	71	80	90	100	110	120	130	140
KF1C								
HSR1	PYNIRNELIKKAHGNFTTQADHLSHIPERIQRQVEVLRNKAVICH-AMHIVASNGKIQQFYDOKATR							
kf1A	TYFAKNTGILKSGEDITFFQSDOVCHIERIERCYNALSNKDALVRCHAYSRLINETQNLIKVMONKTK							
HSR2	KETF-----PCAKADMIVLTDDIIYPPDYVEKMLNFYNSFAFNCTVGINGCTIYDAFDGD-QSKRKV-							
Consensus	KFIILEKLIKENKUGYYITCDDIRYPADYINTMIKKINKYND-KAHGLGHGVIFPSRVANKYFESSURIV-							
	kxi.....lik.ak.d.i....dadi.ypp#y!#.n.n.ns..d..a..g.hg.i.....n...f..sdr-kv.							
	141	150	160	170	180	190	200	210
KF1C								
HSR1	MSVYSSMIKKOIFAIVGGYRASLGADTEFEYEVIMRYGRESIVRLLOPLILGLAGDSGLTRNKGTEALP							
kf1A	LGLITLGYRKVFNEIGFNCTIKASDDEFYHRILKYKGKRINMLFLPLYNTMREDSLFSOH-YENVVD							
HSR2	FSTIQGLLRPVVNQLG---TGTVFLKHUQLPSLKTHAGSQR-FYDVRFSRYHLENETHICVPREKNHLR							
Consensus	YNFQKTRFKOTAYNDLG---TGTVAFRVSIFNKFSLSOFEPHNVDIYFSLCKGNILQVCISRSPSNALI							
	.sf.....k..vvn.lg..tgtv.....d.f.....nd.....vd...fs.y...n.i....c..f...#dl.							
	211	220	230	240	250	260	263	
KF1C								
HSR1	DGYISQSRRREYSIDIAARQVYLKSIYSDKVGRGLLSRYGLFKDVSGLIEQ							
kf1A	ENNIIKQTSQARQNYLHEFQKTHMERKFNELKEIFS-FPRIHADLPISKEDSK							
HSR2	EVS-SGSHEGLNITFKKAPLDI-IKETQIHAGYSKLMLELYTNVEG							
Consensus	EDN-KNT-ETLFHFQNRUEIQSKLITSNPNAGYSSYIPLLNNWANYSELIPC							
	#.n.k.s.e.l...f.....l....i...n....gyss.ypll,n.....se....							



Figure 15B



## Figure 15C

Multalin version 5.4.1

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Published research using this software should cite

Multiple sequence alignment with hierarchical clustering

F. CORPET, 1988, Nucl. Acids Res., 16 (22), 10881-10890

Symbol comparison table: blosum62

Gap weight: 12

Gap length weight: 2

Consensus levels: high=90% low=50%

Consensus symbols:

! is anyone of IV

\$ is anyone of LM

\* is anyone of FY

# is anyone of NDQEBZ

MSF: 651 Check: 0

Name: A Len: 651 Check: 612 Weight: 0.58

Name: B Len: 651 Check: 249 Weight: 0.58

Name: pglA Len: 651 Check: 7677 Weight: 1.08

Name: DcbF Len: 651 Check: 7537 Weight: 1.76

Name: Consensus Len: 651 Check: 5816 Weight: 0.00

//

```

1                                     50
A2 .....MSLFKR ATELFKSGNY KDALTLYENI
B10 .....MSLFKR ATELFKSGNY KDALTLYENI
pglA MKRKKEMTQK QMTKNPPQHE KENELNTFQN KIDSLKTTLN KDIISQQTLL
DcbF .....MSLFKR ATELFKSGNY KDALTLYENI
sensus .....$s1Fkr at#1fKsgny KDaltlyeni

51                                     100
A2 AKIYG....S ESLVKYNIDI CKK.NITQSK SNKIEEDNIS GENKF.....
B10 AKIYG....S ESLVKYNIDI CKK.NITQSK SNKIEEDNIS GENKF.....
pglA AKQDSKHPLS ASLENENKLL LKQLQLVLQE FEKIYTYNQA LEAKLEKDKQ
DcbF AKIYG....S ESLVKYNIDI CKK.NITQSK SNKIEEDNIS GENE.....
Consensus AKiyg....S eSLvkyNidi cKk.#itqsk s#K1eedNis gEnkf.....

101                                    150
A2 SVSIKDLYNE ISNSELGITK ERLGAPPLVS IIMTSHNTEK FIEASINSLL
B10 SVSIKDLYNE ISNSELGITK ERLGAPPLVS IIMTSHNTEK FIEASINSLL
pglA TTSITDLYNE VAKSDLGLVK ETNSVNPLVS IIMTSHNTAQ FIEASINSLL
DcbF SVSIKDLYNE ISNSELGITK ERLGAPPLVS IIMTSHNTEK FIEASINSLL
Consensus svSIkDLYNE !snS#LGitK ErlgapPLVS IIMTSHNTek FIEASINSLL

151                                    200
A2 LQTYNNLEVI VDDYSTDKT FQIASRIANS TSKVKTFRNL SNLGTYFAKN
B10 LQTYNNLEVI VDDYSTDKT FQIASRIANS TSKVKTFRNL SNLGTYFAKN
pglA LQTYKNIEII IVDDSSDNT FEIASRIANT TSKVRVFRNL SNLGTYFAKN
DcbF LQTYNNLEVI VDDYSTDKT FQIASRIANS TSKVKTFRNL SNLGTYFAKN
Consensus LQTYnN1E!I !VDDyStDkt F#IASRIANS TSKVktFRNL SNLGTYFAKN
  
```

## Fig. 15C cont'd

201					250
A2	TGILKSKGDI	IFFQSDDDVC	HHERIERCVN	ALLSNKDNIA	VRCAYSRLNL
B10	TGILKSKGDI	IFFQSDDDVC	HHERIERCVN	ALLSNKDNIA	VRCAYSRLNL
pg1A	TGILKSKGDI	IFFQSDDDVC	HHERIERCVN	ILLANKETIA	VRCAYSRLAP
DcbF	TGILKSKGDI	IFFQSDDDVC	HHERIERCVN	ALLSNKDNIA	VRCAYSRLNL
Consensus	TGILKSKGDI	IFFQSDDDVC	HHERIERCVN	aLLsNK#nIA	VRCAYSRLnl
251					300
A2	ETQNIIVND	NKYKLGLITL	GVYRKVFNEI	GFFNCTTKAS	DDEFYHRIIK
B10	ETQNIIVND	NKYKLGLITL	GVYRKVFNEI	GFFNCTTKAS	DDEFYHRIIK
pg1A	ETQNIIVNN	MDYRLGFITL	GMHRKVQEI	GFFNCTTKGS	DDEFFHRIAK
DcbF	ETQNIIVND	NKYKLGLITL	GVYRKVFNEI	GFFNCTTKAS	DDEFYHRIIK
Consensus	ETQNIIVN#	nkYkLGLITL	GvyRKVF#EI	GFFNCTTKaS	DEFF#HRIiK
301					350
A2	YYGKNRINNL	FLPLYNTMR	EDSLFSDMVE	WVDENNIKQK	TSDARQNYLH
B10	YYGKNRINNL	FLPLYNTMR	EDSLFSDMVE	WVDENNIKQK	TSDARQNYLH
pg1A	YYGKEKIKNL	LLPLYNTMR	ENSLFTDMVE	WIDNHNIIQK	MSDTRQHYAT
DcbF	YYGKNRINNL	FLPLYNTMR	EDSLFSDMVE	WVDENNIKQK	TSDARQNYLH
Consensus	YYGK#rInNL	fLPLYNTMR	E#SLFsDMVE	WID#nNikQK	tSDaRqNyLh
351					400
A2	EFQKIHNERK	LNELKEIFSF	PRIHDALPIS	KEMSKLSNPK	IPVYINICSI
B10	EFQKIHNERK	LNELKEIFSF	PRIHDALPIS	KEMSKLSNPK	IPVYINICSI
pg1A	LFQAMHNETA	SHDFKNLFQF	PRIYDALPVP	QEMSKLSNPK	IPVYINICSI
DcbF	EFQKIHNERK	FNELKEIFSF	PRIHDALPIS	KEMSKLSNPK	IPVYINICSI
Consensus	efQkIHNErk	.n#lK#iFsF	PRIhDALP!s	kEMSKLSNPK	IPVYINICSI
401					450
A2	PSRIKQLQYT	IGVLKNQCDH	FHIYLDGYPE	VPDFIKKLGN	KATVINCONK
B10	PSRIKQLQYT	IGVLKNQCDH	FHIYLDGYPE	VPDFIKKLGN	KATVINCONK
pg1A	PSRIAQLRRI	IGILKNQCDH	FHIYLDGYVE	IPDFIKNLGN	KATVVHCKDK
DcbF	PSRIKQLQYT	IGVLKNQCDH	FHIYLDGYPE	VPDFIKKLGN	KATVINCONK
Consensus	PSRIkQLqyt	IG!LKNQCDH	FHIYLDGYpe	!PDFIKkLGN	KATV!nCq#K
451					500
A2	NESIRDNGKF	ILLEKLIKEN	KDGYIITCDD	DIRYPADYTN	TMIKKINKYN
B10	NESIRDNGKF	ILLEKLIKEN	KDGYIITCDD	DIRYPADYIN	TMIKKINKYN
pg1A	DNSIRDNGKF	ILLEELIEKN	QDGYIITCDD	DIIYPSDYIN	TMIKKLNEYD
DcbF	NESIRDNGKF	ILLEKLIKEN	KDGYIITCDD	DIRYPADYIN	TMIKKINKYN
Consensus	##SIRDNGKF	ILLEkLIken	kDGYIITCDD	DirYPaDYiN	TMIKKiNky#
501					550
A2	DKAAIGLHGV	IFPSRVNKYF	SSDRIVYNFQ	KPLENDTAVN	ILGTGTVAFR
B10	DKAAIGLHGV	IFPSRVNKYF	SSDRIVYNFQ	KPLENDTAVN	ILGTGTVAFR
pg1A	DKAVIGLHGI	LFPSRMTKYF	SADRLVYSFY	KPLEKDKAVN	VLGTGTVSFR
DcbF	DKAAIGLHGV	IFPSRVNKYF	SSDRIVYNFQ	KTFRK.....	.....
Consensus	DKAAIGLHG!	iFPSRvnKYF	SsDRiVYnFq	Kplekd.avn	.lgtgtv.fr
551					600
A2	VSIFNKFSLS	DFEHPGMVDI	YFSILCKKNN	ILQVCISRPS	NWLTEDNKNT
B10	VSIFNKFSLS	DFEHPGMVDI	YFSILCKKNN	ILQVCISRPS	NWLTEDNKNT
pg1A	VSLFNQFSLS	DFTHSGMADI	YFSLLCKKNN	ILQICISRPA	NWLTEDNRDS
DcbF	.....	.....	.....	.....	.....
Consensus	vs.fn.fsIs	df.h.gm.di	yfs.lckknn	ilq.cisrp.	nwltedn...

# Fig. 15C c nt'd

```

601                                     650
A2  ETLFHEFQNR DEIQSKLIIS NNPWGYSSIIY PLLNNNANYS ELIPCLSFYN
B10 ETLFHEFQNR DEIQSKLIIS NNPWGYSSIIY PLLNNNANYS ELIPCLSFYN
pglA ETLYHQYRDN DEQQTQLIME NGPWGYSSIIY PLVKNHPKFT DLIPCLPFYF
DcbF .....
Consensus etl.h..... de.q..li.. n.pwgyssiy pl..n..... .lipcl.fy.

```

```

651
A2  E
B10 E
pglA L
DcbF .
Consensus .

```

## Figure 15D

Multalin version 5.4.1

Copyright I.N.R.A. France 1989, 1991, 1994, 1996

Published research using this software should cite

Multiple sequence alignment with hierarchical clustering

F. CORPET, 1988, Nucl. Acids Res., 16 (22), 10881-10890

Symbol comparison table: blosum62

Gap weight: 12

Gap length weight: 2

Consensus levels: high=90% low=50%

Consensus symbols:

! is anyone of IV

\$ is anyone of LM

% is anyone of FY

# is anyone of NDQEBZ

MSF: 651 Check: 0

Name: pmHS Len: 651 Check: 612 Weight: 0.75

Name: pgLA Len: 651 Check: 7677 Weight: 0.75

Name: DcbF Len: 651 Check: 7537 Weight: 1.49

Name: Consensus Len: 651 Check: 5816 Weight: 0.00

//

```

1                                     50
pmHS .....MSLFKR ATELFKSGNY KDALTLYENI
pgLA MKRKKEMTQK QMTKNPPQHE KENELNTFQN KIDSLKTTLN KDIIISQQTLL
DcbF .....MSLFKR ATELFKSGNY KDALTLYENI
Consensus .....$sLFkr at#lFksgny KDaltlyeni

51                                     100
pmHS AKIYG....S ESLVKYNIDI CKK.NITQSK SNKIEEDNIS GENKF.....
pgLA AKQDSKHPLS ASLENENKLL LKQLQLVLQE FEKIITYNQA LEAKLEKDKQ
DcbF AKIYG....S ESLVKYNIDI CKK.NITQSK SNKIEEDNIS GENE.....
Consensus AKIyg....S eSLvkyNidi cKk.#itqsk s#KieedNis gEnkf.....

101                                    150
pmHS SVSIKDLYNE ISNSELGITK ERLGAPPLVS IIMTSHNTEK FIEASINSLL
pgLA TTSITDLYNE VAKSDLGLVK ETNSVNPLVS IIMTSHNTAQ FIEASINSLL
DcbF SVSIKDLYNE ISNSELGITK ERLGAPPLVS IIMTSHNTEK FIEASINSLL
Consensus svSikDLYNE !sn$LGitK ErlgapPLVS IIMTSHNtek FIEASINSLL

151                                    200
pmHS LQTYNNLEVI VDDYSTDKT FQIASRIANS TSKVKTFRNL SNLGTYFAKN
pgLA LQTYKNIEII IVDDSSDNT FEIASRIANT TSKVRVFRNL SNLGTYFAKN
DcbF LQTYNNLEVI VDDYSTDKT FQIASRIANS TSKVKTFRNL SNLGTYFAKN
Consensus LQTYnNle!I !VDDyStDkt F#IASRIANS TSKVktFRNL SNLGTYFAKN

201                                    250
pmHS TGILKSKGDI IFFQSDDDVC HHERIERCVN ALLSNKDNIA VRCAYSRLNL
pgLA TGILKSKGDI IFFQSDDDVC HHERIERCVN ILLANKETIA VRCAYSRLAP
DcbF TGILKSKGDI IFFQSDDDVC HHERIERCVN ALLSNKDNIA VRCAYSRLNL
Consensus TGILKSKGDI IFFQSDDDVC HHERIERCVN aLLsNK#nIA VRCAYSRLnl

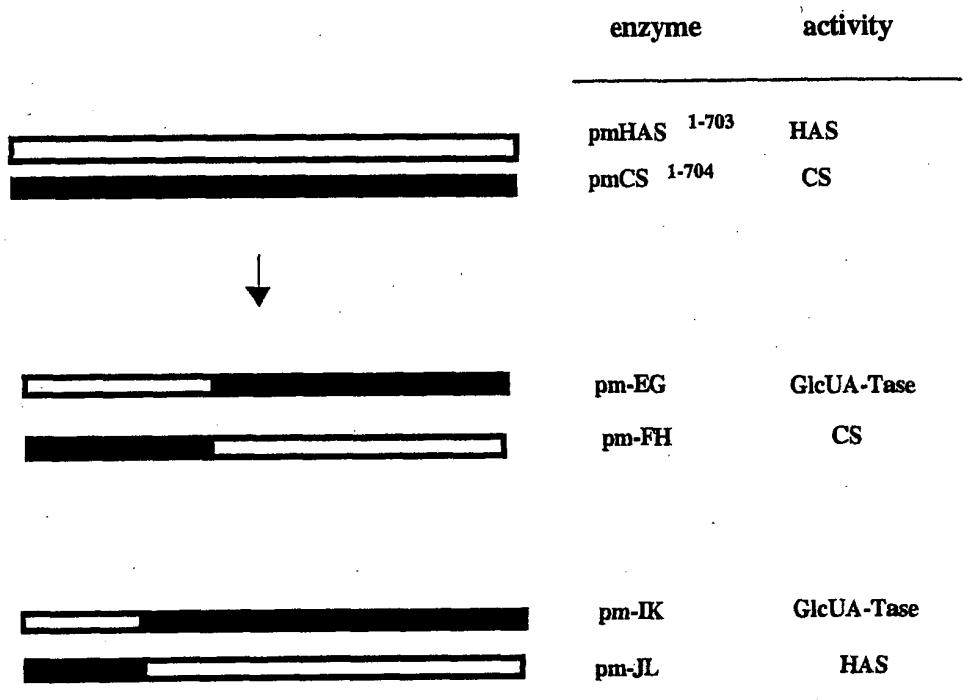
251                                    300
pmHS ETQNIIVKND NKYKLGITL GYRKVFNEI GFFNCTTKAS DDEFYHRIIK
pgLA ETQHIIKVN MDYRLGFITL GMHRKVFQEI GFFNCTTKGS DDEFFHRIAK
DcbF ETQNIIVKND NKYKLGITL GYRKVFNEI GFFNCTTKAS DDEFYHRIIK
Consensus ETQnIIVKVN# nkYKLGITL GvyRKVF#EI GFFNCTTKaS DDEF#HRIiK

```

## Figure 15D

	301		350
pmHS	YYGKNRINNL	FLPLYNTMR	EDSLFSDMVE WVDENNIKQK TSDARQNYLH
pglA	YYGKEKIKNL	LLPLYNTMR	ENSLFTDMVE WIDNHNIIQK MSDTRQHYAT
DcbF	YYGKNRINNL	FLPLYNTMR	EDSLFSDMVE WVDENNIKQK TSDARQNYLH
Consensus	YYGK#rInNL	flPLYNTMR	E#SLFsDMVE W!D#nNIkQK tSDaRQnYlH
	351		400
pmHS	EFQKIHNERK	LNELKEIFSF	PRIHDALPIS KEMSKLSNPK IPVYINICSI
pglA	LFQAMHNETA	SHDFKNLFQF	PRIYDALPVP QEMSKLSNPK IPVYINICSI
DcbF	EFQKIHNERK	FNELKEIFSF	PRIHDALPIS KEMSKLSNPK IPVYINICSI
Consensus	eFQkiHNErk	.n#lK#iFsF	PRIHDALP!s KEMSKLSNPK IPVYINICSI
	401		450
pmHS	PSRIKQLQYT	IGVLKNQCDH	FHIYLDGYPE VPDFIKKLGN KATVINCONK
pglA	PSRIAQLRRI	IGILKNQCDH	FHIYLDGYVE IPDFIKNLGN KATVVHCKDK
DcbF	PSRIKQLQYT	IGVLKNQCDH	FHIYLDGYPE VPDFIKKLGN KATVINCONK
Consensus	PSRIkQLqyt	IG!LKNQCDH	FHIYLDGYpe !PDFIKKLGN KATV!nCq#K
	451		500
pmHS	NESIRDNGKF	ILLEKLIKEN	KDGYITCDD DIRYPADYTN TMIKKINKYN
pglA	DNSIRDNGKF	ILLEELIEKN	QDGYITCDD DIIYPSDYIN TMIKKLNEYD
DcbF	NESIRDNGKF	ILLEKLIKEN	KDGYITCDD DIRYPADYIN TMIKKINKYN
Consensus	##SIRDNGKF	ILLEkLIkEn	kDGYITCDD DirYPaDYiN TMIKKiNkY#
	501		550
pmHS	DKAAIGLHGV	IFPSRVNKYF	SSDRIVYNFQ KPLENDTAVN ILGTGTVAFR
pglA	DKAVIGLHGI	LFPSRMTKYF	SADRLVYSFY KPLEKD KAVN VLGTGTVSFR
DcbF	DKAAIGLHGV	IFPSRVNKYF	SSDRIVYNFQ KTFRK.....
Consensus	DKAAaIGLHG!	iFPSRvnKYF	SsDRiVYnFq Kplekd.avn .lgtgtv.fr
	551		600
pmHS	VSIFNKFSLS	DFEHPGMVDI	YFSILCKKNN ILQVCISRPS NWLTEDNKNT
pglA	VSLFNQFSLS	DFTHSGMADI	YFSLLCKKNN ILQICISRPA NWLTEDNRDS
DcbF	.....	.....	.....
Consensus	vs.fn.fsIs	df.h.gm.di	yfs.lckknn ilq.cisrp. nwltedn...
	601		650
pmHS	ETLFHEFQNR	DEIQSKLIIS	NNPWGYSSII PLLNNNANYS ELIPCLSFYN
pglA	ETLYHQYRDN	DEQQTQLIME	NGPWGYSSII PLVKNHPKFT DLIPCLPFYF
DcbF	.....	.....	.....
Consensus	etl.h.....	de.q..li..	n.pwgyssiy pl..n..... .lipcl.fy.
	651		
pmHS	E		
pglA	L		
DcbF	.		
Consensus	.		

**Figure 16**

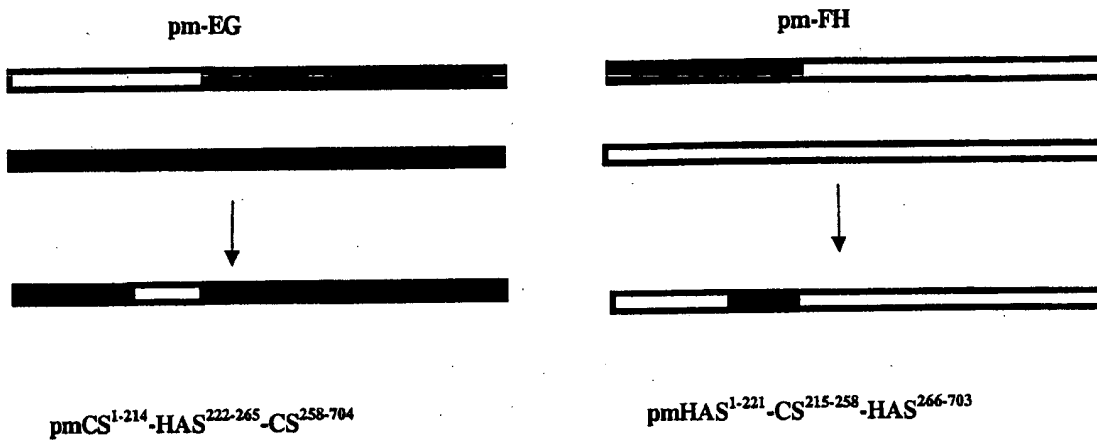


**Figure 17**


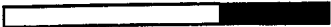






	211	220	230	240	250
	-----+-----+-----+-----+				
<b>PnHAS</b>	NKLDIRYYRQKDNQGFQASARNMGLRLAKYDFIGLLDCDH				
<b>PnCS</b>	QKLDIKYYRQKDYGYQLCAVRNLGLRTAKYDFYSILDCDH				
<b>Turkey</b>	EKLDIKYYRQKDYGYQLCAVRNLGLRTAKYDFYSILDCDH				
<b>Goose</b>	YDIKYYRQKDYGYQLCAVRNLGLRTAKYDFYSILDC				
<b>Sea-lion</b>	KYYRQKDYGYQLCAVRNLGLRTAKYDFYSILDC				
<b>Consensus</b>	...dikYYRQKDYGYQLCAVRNLGLRTAKYDF!siLDC...				
		-	-		-
mutant 1		★			
mutant 2			★		
mutant 3			★		
mutant 4		★	★		
mutant 5		★	★		
mutant 6			★★		
mutant 7		★	★★		
mutant 8				★	
mutant 9				★★★	



**Figure 18**



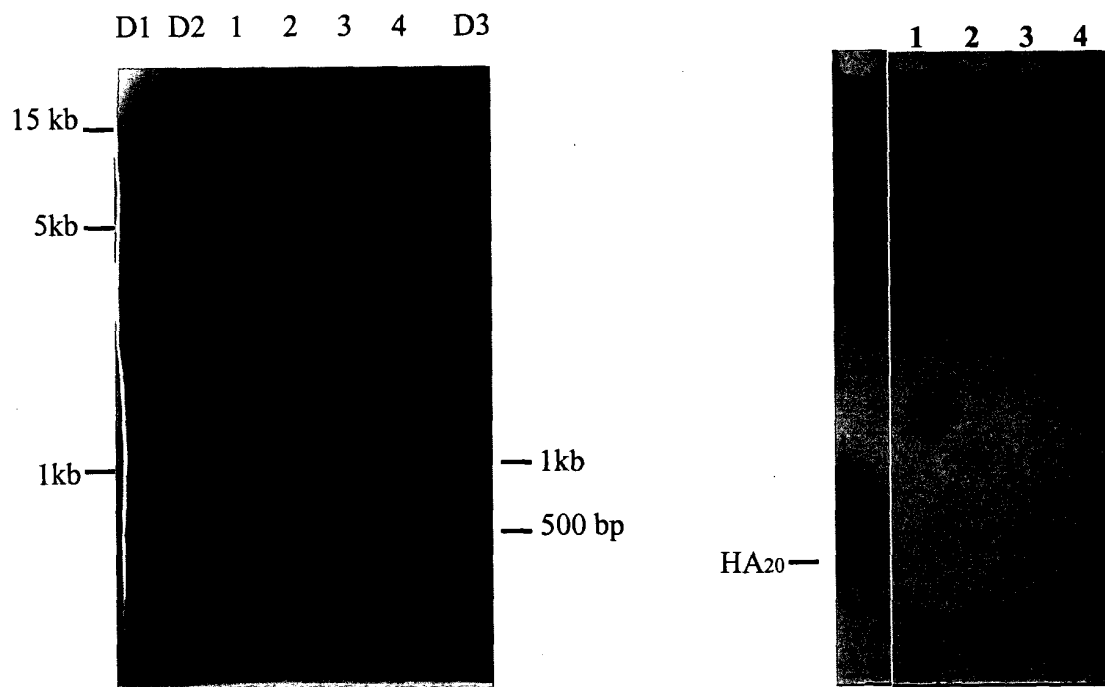
**Figure 19**

	activity		
	HAS	CS	GlcUA-Tase
	-	+	<input checked="" type="checkbox"/>
	+	-	<input checked="" type="checkbox"/>
	-	+	+
	-	-	+
	+	-	+
	-	-	+
	+	+	+
	not expressed		

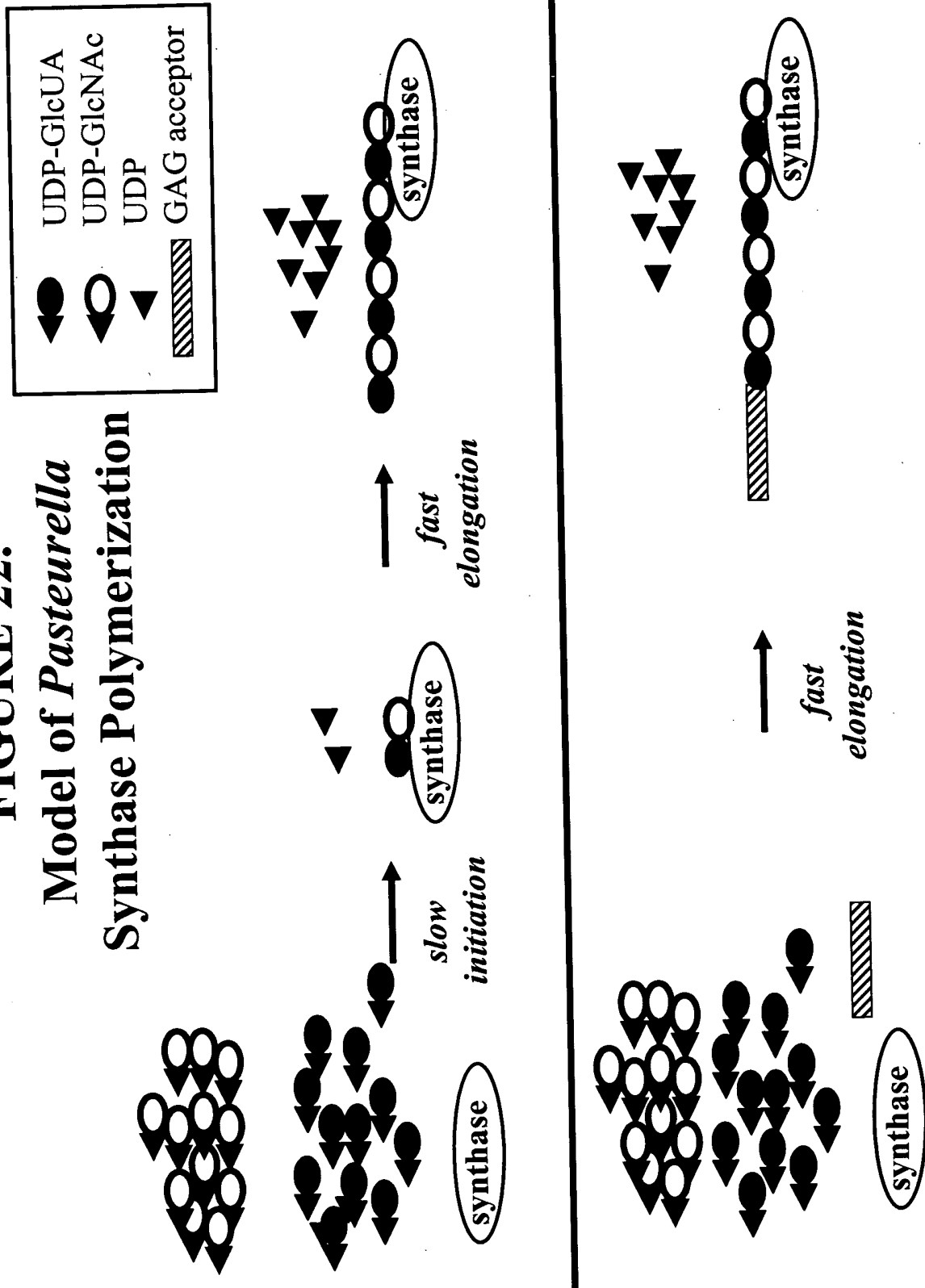
**FIGURE 20**



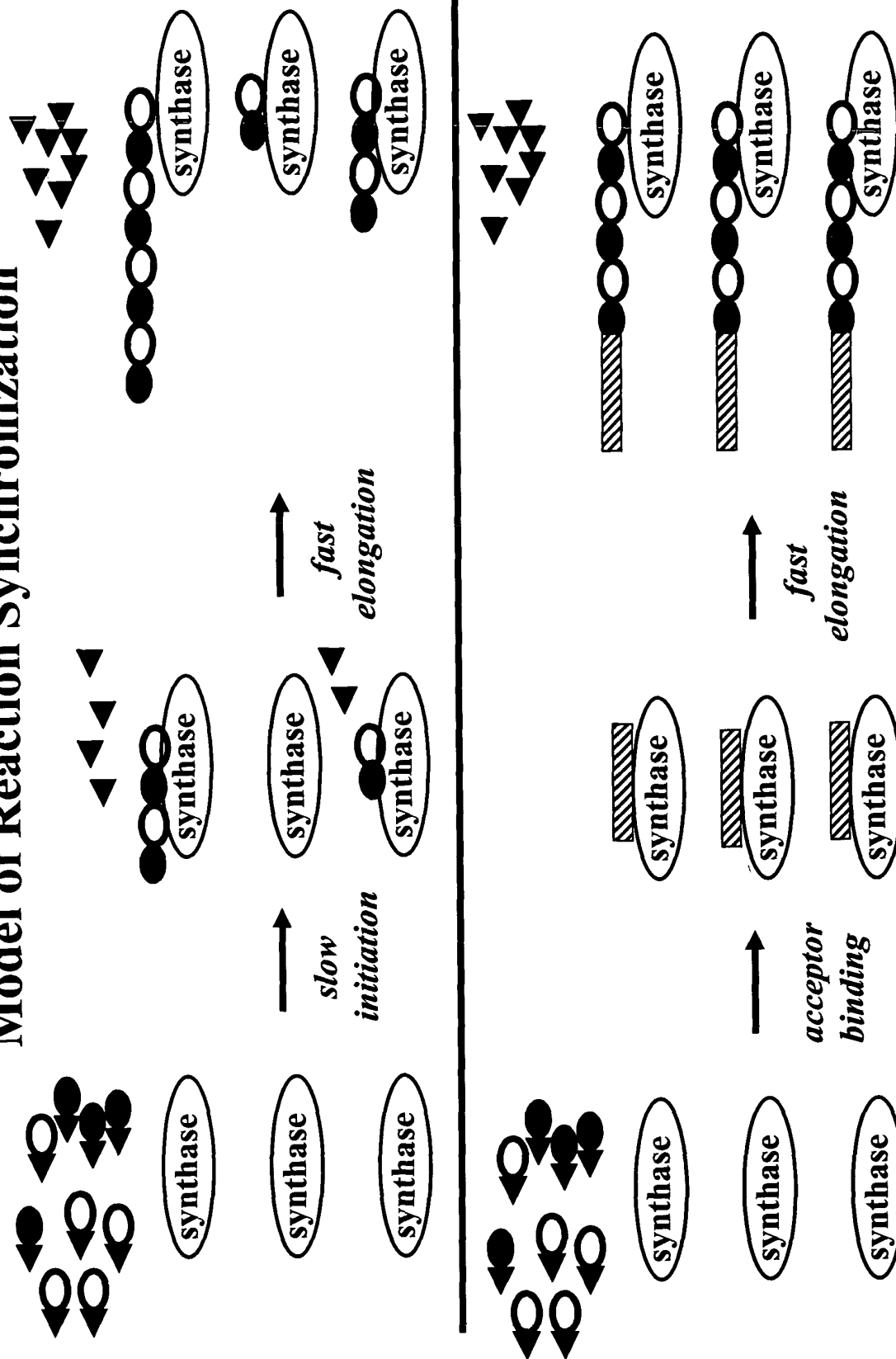
FIGURE 21



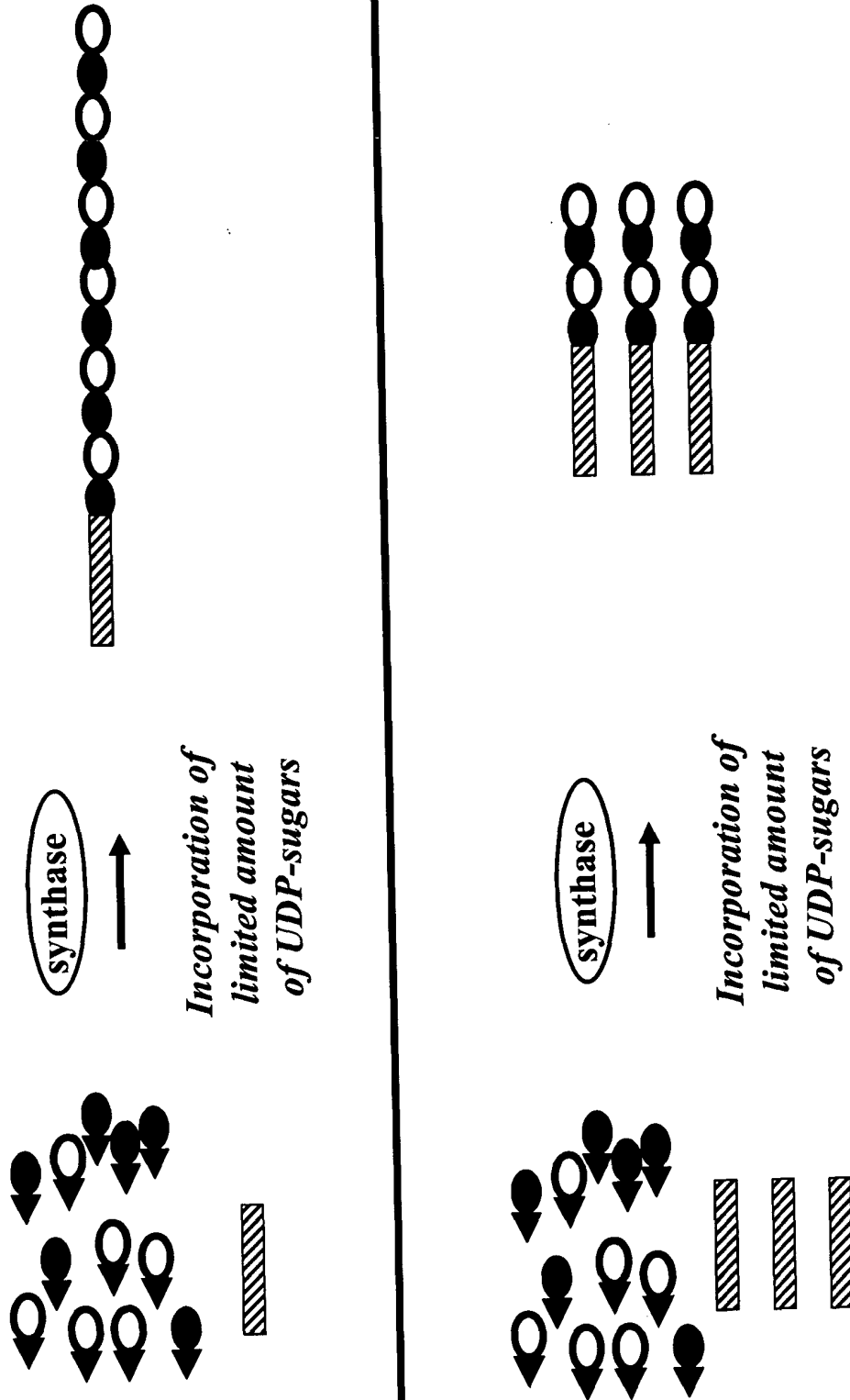
**FIGURE 22.**  
**Model of *Pasteurella***  
**Synthase Polymerization**



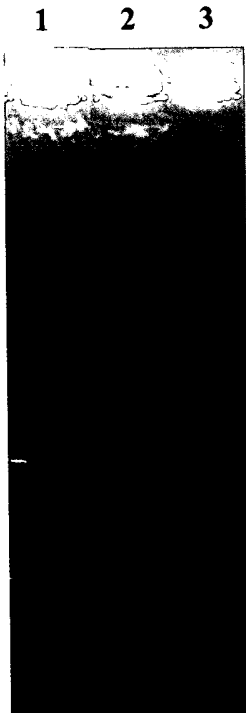
**FIGURE 23.**  
**Model of Reaction Synchronization**



**FIGURE 24.**  
**Model of Stoichiometric Control of Polymer Size**

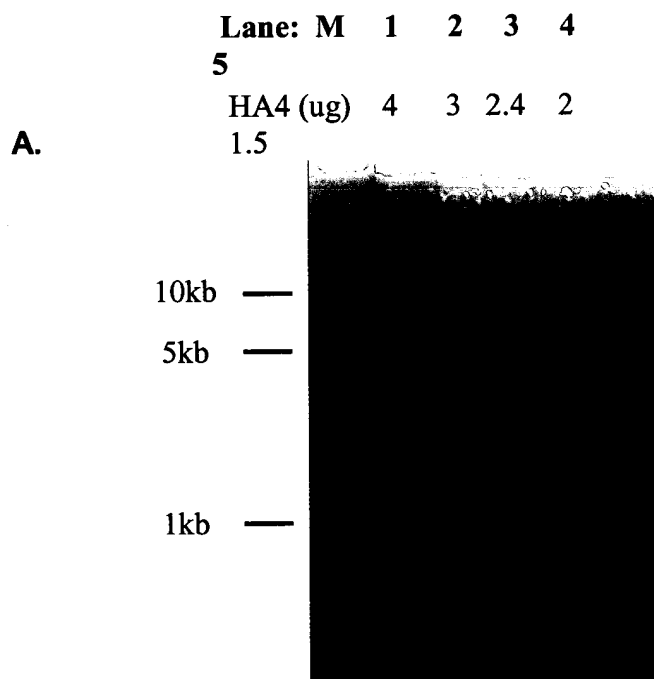


**FIGURE 25**





**FIGURE 26**



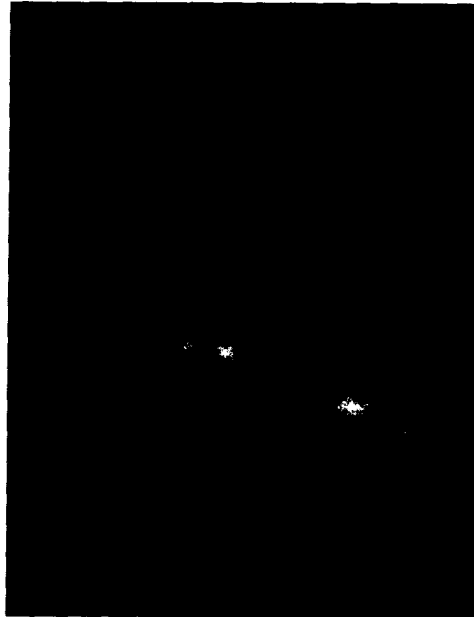
**B.**

<b>Sample No</b>	<b><i>M<sub>n</sub></i></b>	<b><i>M<sub>w</sub></i></b>	<b>polydispersity</b>
<b>#1</b>	<b>283400</b>	<b>283800</b>	<b>1.001</b>
<b>#2</b>	<b>346400</b>	<b>347000</b>	<b>1.002</b>
<b>#3</b>	<b>422200</b>	<b>423700</b>	<b>1.004</b>
<b>#4</b>	<b>490000</b>	<b>493100</b>	<b>1.006</b>
<b>#5</b>	<b>569700</b>	<b>575200</b>	<b>1.010</b>

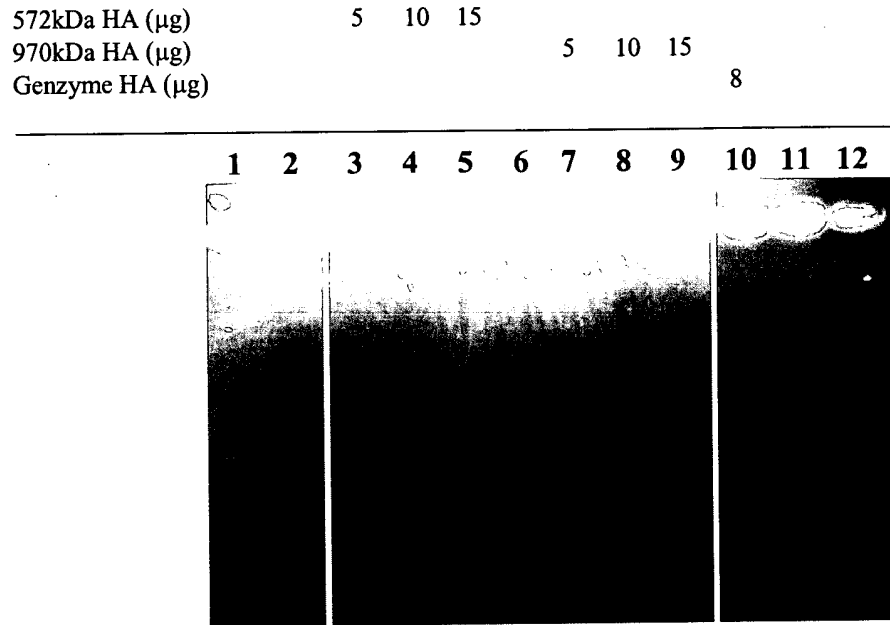
Express Mail No.: EV272909140US Deposited: 08/15/2003  
Title: TARGETED GLYCOSAMINOGLYCAN POLYMERS BY  
POLYMER GRAFTING AND METHODS OF MAKING AND USING  
SAME  
Inventors: Paul L. DeAngelis et al. Group: Unknown  
Filed: Herewith Examiner: Unknown  
Agent: Douglas J. Sorocco Dkt. No.: 3554,097  
SHEET 34 OF 41 Formal Drawings

## FIGURE 27

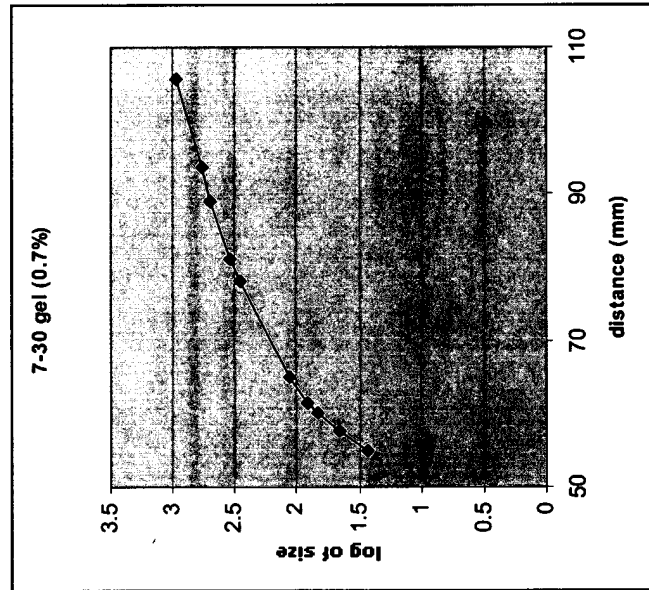
1 2 3 4 5 6 7



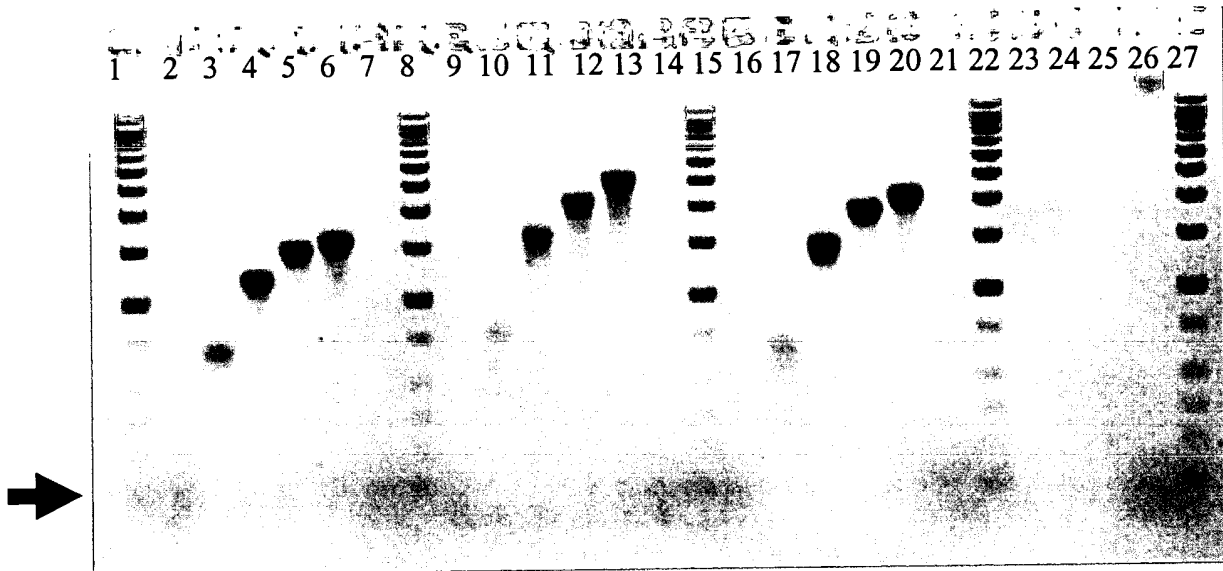
## FIGURE 28



**FIGURE 29.**  
**Agarose Gels of Ladders and Migration**

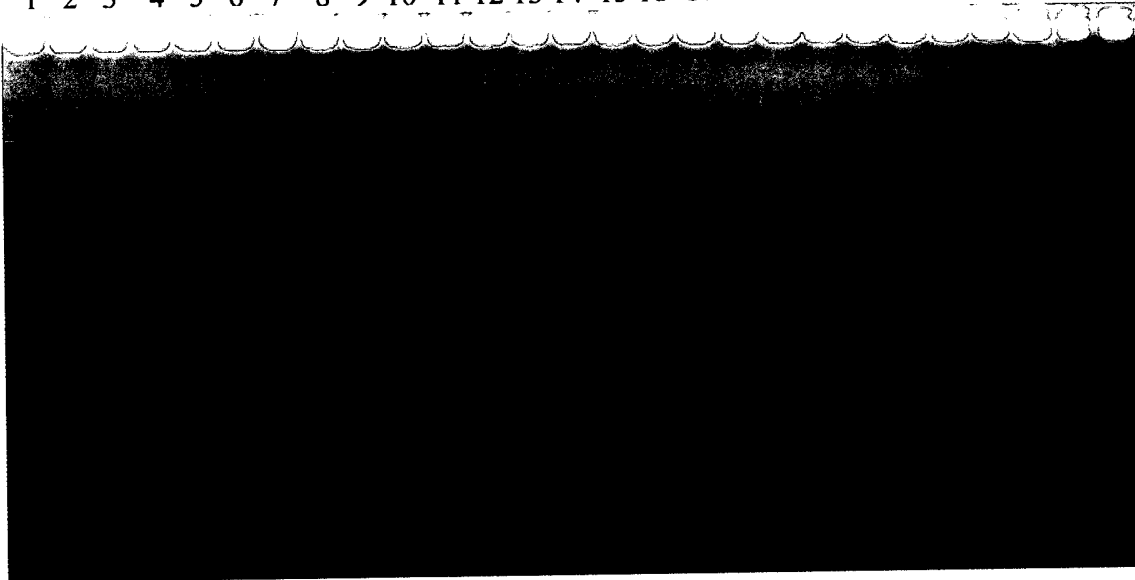


**FIGURE 30**

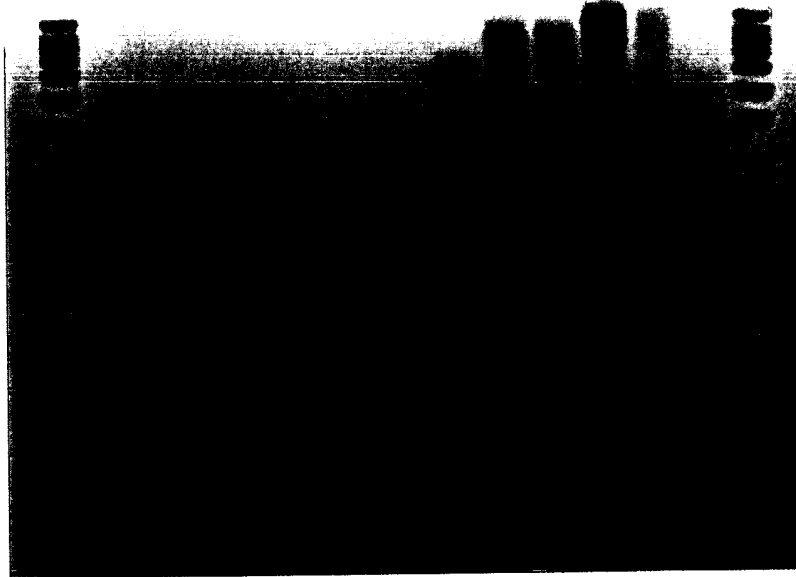


## FIGURE 31

1 2 3 4 5 6 7 8 9 10 11 12 13 14 15 16 17 18 19 20 21 22 23 24 25 26



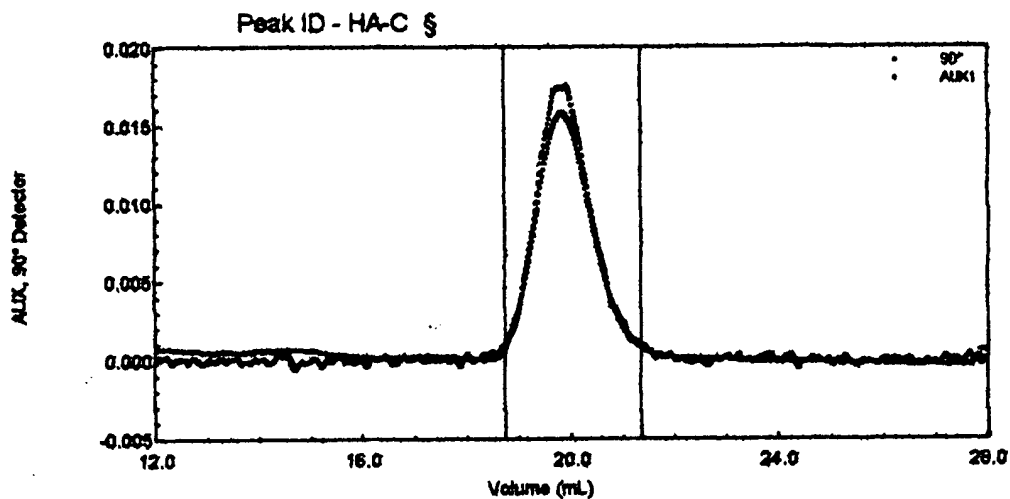
## FIGURE 32



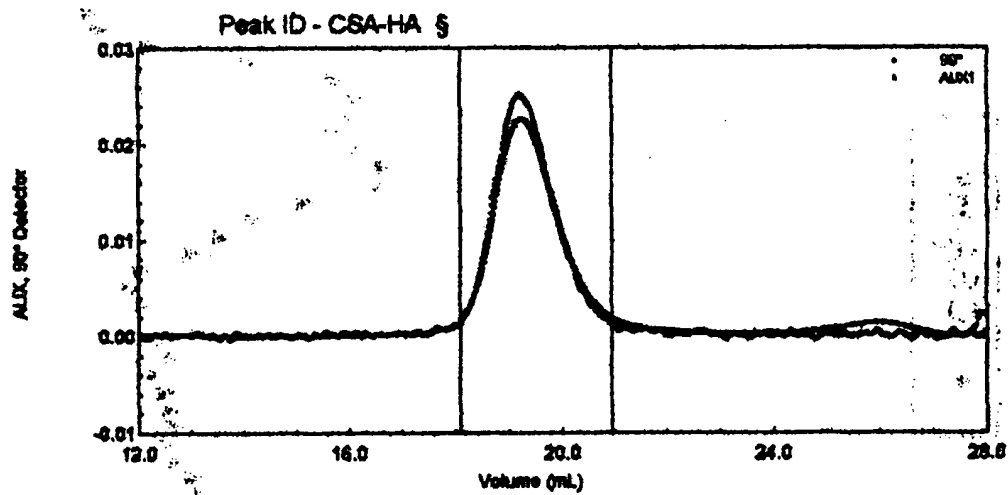
Time:	0	2	4	4	6	O/N	0
Feeding round:	-	1	2	1	3	3	-

FIGURE 33

A.



B.





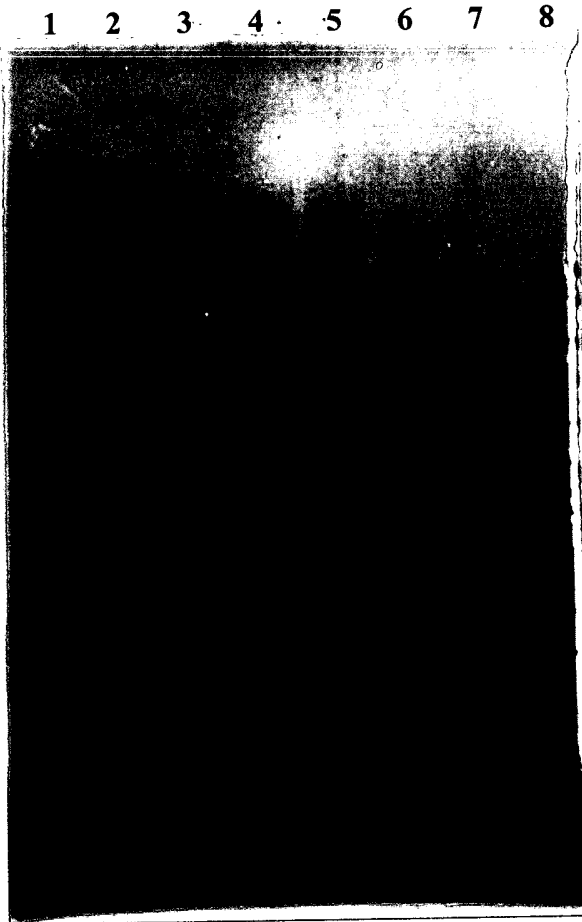


FIG. 34